

ENTERED

nch *A. Kobel, k*
 H14.
 1638

- ENTERED

#14 16387

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

☐ Deleted extra, invalid, headings used by an applicant, specifically:

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☒ Other: Entered "hard returns" to correct sequences
17, 25, 28.

*Examiner: ~~The above~~ corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\03052001\I271584A.raw

4 <110> APPLICANT: BLUMWALD, Eduardo
5 APSE, Maris
6 SNEDDEN, Wayne
7 AHARON, Gilad
9 <120> TITLE OF INVENTION: GENETIC ENGINEERING SALT TOLERANCE IN CROP PLANTS

W--> 0 <130> FILE REFERENCE:

11 <140> CURRENT APPLICATION NUMBER: US 09/271,584A
12 <141> CURRENT FILING DATE: 1999-03-18
14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00219
15 <151> PRIOR FILING DATE: 1999-03-18
17 <150> PRIOR APPLICATION NUMBER: US 60/078,474
18 <151> PRIOR FILING DATE: 1998-04-01
20 <150> PRIOR APPLICATION NUMBER: US 60/116,111
21 <151> PRIOR FILING DATE: 1999-01-15
23 <160> NUMBER OF SEQ ID NOS: 37
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28 <211> LENGTH: 2178
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34 <222> LOCATION: (286)..(1899)'
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43 ttgattacc cagaagttgt tcaaggaatg gtttcagtgg acagcagcga aagataaaaag 180
45 agactttttt ttccagattt tgctgatcca aaatctgaat agttgttcat gttcttggat 240
47 caaatctgga aagaggaagt ttgttgatc tagaagaaga taaca atg ttg gat tct 297
Met Leu Asp Ser
1
51 cta gtg tcg aaa ctg cct tcg tta tcg aca tct gat cac gct tct gtg 345
52 Leu Val Ser Lys Leu Pro Ser Leu Ser Thr Ser Asp His Ala Ser Val
53 5 10 15 20
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56 Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala Cys Ile Val Leu
57 25 30 35
59 ggt cat ctt ttg gaa gag aat aga tgg atg aac gaa tcc atc acc gcc 441
60 Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu Ser Ile Thr Ala
61 40 45 50
63 ttg ttg att ggg cta ggc act ggt gtt acc att ttg ttg att agt aaa 489
64 Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu Leu Ile Ser Lys
65 55 60 65
67 gga aaa agc tcg cat ctt ctc gtc ttt agt gaa gat ctt ttc ttc ata 537
68 Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp Leu Phe Phe Ile
69 70 75 80

see p. 5

RECEIVED
MAR 07 2001
TECH CENTER 1600/2900

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75 aag caq ttt ttc cgc aat ttc qtg act att atq ctt ttt ggt gct gtt 633
76 Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu Phe Gly Ala Val
77 105 110 115
79 ggg act att att tct tgc aca atc ata tct cta ggt gta aca cag ttc 681
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81 120 125 130
83 ttt aag aag ttg gac att gga acc ttt gac ttg ggt gat tat ctt gct 729
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85 135 140 145
87 att ggt gcc ata ttt gct gca aca gat tca gta tgt aca ctg cag gtt 777
88 Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys Thr Leu Gln Val
89 150 155 160
91 ctg aat caa gac gag aca cct ttg ctt tac agt ctt gta ttc gga gag 825
92 Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu Val Phe Gly Glu
93 165 170 175 180
95 ggt gtt gtg aat gat gca acg tca gtt gtg gtc ttc aac gcg att cag 873
96 Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe Asn Ala Ile Gln
97 185 190 195
99 agc ttt gat ctc act cac cta aac cac gaa gct gct ttt cat ctt ctt 921
100 Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala Phe His Leu Leu
101 200 205 210
103 gga aac ttc ttg tat ttg ttt ctc cta agt acc ttg ctt ggt gct gca 969
104 Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu Leu Gly Ala Ala
105 215 220 225
107 acc ggt ctg ata agt gcg tat gtt atc aag aag cta tac ttt gga agg 1017
108 Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu Tyr Phe Gly Arg
109 230 235 240
111 cac tca act gac cga gag gtt gcc ctt atg atg ctt atg gcg tat ctt 1065
112 His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu Met Ala Tyr Leu
113 245 250 255 260
115 tct tat atg ctt gct gag ctt ttc gac ttg agc ggt atc ctc act gtg 1113
116 Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly Ile Leu Thr Val
117 265 270 275
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121 280 285 290
123 gag agc tca aga ata aca aca aag cat acc ttt gca act ttg tca ttt 1209
124 Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala Thr Leu Ser Phe
125 295 300 305
127 ctt gcg gag aca ttt att ttc ttg tat gtt gga atg gat gcc ttg gac 1257
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132 Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly Thr Ser Ile Ala
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RAW SEQUENCE LISTING

DATE: 03/05/2001

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140 Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys Lys Asn Gln Ser
141          360          365          370
143 gag aaa atc aac ttt aac atg cag gtt gtg att tgg tgg tct ggt ctc 1449
144 Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp Trp Ser Gly Leu
145          375          380          385
147 atg aga ggt gct gta tct atg gct ctt gca tac aac aag ttt aca agg 1497
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149          390          395          400
151 gcc ggg cac aca gat gta cgc ggg aat gca atc atg atc acg agt acg 1545
152 Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met Ile Thr Ser Thr
153 405          410          415          420
155 ata act gtc tgt ctt ttt agc aca gtg gtg ttt ggt atg ctg acc aaa 1593
156 Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly Met Leu Thr Lys
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159 cca ctc ata agc tac cta tta ccg cac cag aac gcc acc acg agc atg 1641
160 Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala Thr Thr Ser Met
161          440          445          450
163 tta tct gat gac aac acc cca aaa tcc ata cat atc cct ttg ttg gac 1689
164 Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile Pro Leu Leu Asp
165          455          460          465
167 caa gac tct ttc att gag cct tca ggg aac cac aat gty cct cgg cct 1737
168 Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn Val Pro Arg Pro
169          470          475          480
171 gac agt ata cgt ggc ttc ttg aca cgg ccc act cga acc gtg cat tac 1785
172 Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg Thr Val His Tyr
173 485          490          495          500
175 tac tgg aga caa ttt gat gac tcc ttc atg cga ccc gtc ttt gga ggt 1833
176 Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly
177          505          510          515
179 cgt ggc ttt gta ccc ttt gtt cca ggt tct cca act gag aga aac cct 1881
180 Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu Arg Asn Pro
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185          535
187 ttttttggta gaaaaggtg attcaaatat tgcttttgtg taaattatcc atttgtaata 1989
189 ttgtttgtga ggacagaaat ctgtcctaac gttttgagag cagaaagcaa aacatggcaa 2049
191 ctttgaagtg tttgattgat gtatgtaatt atattcataa ttgttttgtt gtaacacaaa 2109
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201 <213> ORGANISM: Arabidopsis thaliana
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Figure 1(a)

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211	His	Ala	Ser	Val	Val	Ala	Leu	Asn	Leu	Phe	Val	Ala	Leu	Leu	Cys	Ala			
212				20					25					30					
214	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp	Met	Asn	Glu			
215			35					40					45						
217	Ser	Ile	Thr	Ala	Leu	Leu	Ile	Gly	Leu	Gly	Thr	Gly	Val	Thr	Ile	Leu			
218		50					55					60							
220	Leu	Ile	Ser	Lys	Gly	Lys	Ser	Ser	His	Leu	Leu	Val	Phe	Ser	Glu	Asp			
221	65					70					75				80				
223	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn	Ala	Gly	Phe			
224				85					90					95					
226	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Val	Thr	Ile	Met	Leu			
227			100						105					110					
229	Phe	Gly	Ala	Val	Gly	Thr	Ile	Ile	Ser	Cys	Thr	Ile	Ile	Ser	Leu	Gly			
230			115					120					125						
232	Val	Thr	Gln	Phe	Phe	Lys	Lys	Leu	Asp	Ile	Gly	Thr	Phe	Asp	Leu	Gly			
233		130					135					140							
235	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp	Ser	Val	Cys			
236	145					150				155				160					
238	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu	Tyr	Ser	Leu			
239				165					170					175					
241	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Val	Phe			
242			180					185					190						
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245			195				200					205							
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248		210					215					220							
250	Leu	Gly	Ala	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Tyr	Val	Ile	Lys	Lys	Leu			
251	225					230				235				240					
253	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu	Met	Met	Leu			
254				245					250					255					
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257			260						265				270						
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284 405 410 415
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287 420 425 430
289 Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
290 435 440 445
292 Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
293 450 455 460
295 Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
296 465 470 475 480
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327 1 5 10 15
329 cat cct cag gtg ata cca atc tca gtg ttc atc gcc att ctc tgt cta 156
330 His Pro Gln Val Ile Pro Ile Ser Val Phe Ile Ala Ile Leu Cys Leu
331 20 25 30
333 tgt tta gtt atc ggc cac ttg ctt gaa gag aat cga tgg gtt aat gaa 204
334 Cys Leu Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Val Asn Glu
335 35 40 45
337 tct att acc gcc att tta gta gga gca gca tca gga aca gtg atc tta 252
338 Ser Ile Thr Ala Ile Leu Val Gly Ala Ala Ser Gly Thr Val Ile Leu
339 50 55 60
341 ctt att agt aaa gga aaa agt tca cat att ttg gtg ttt gat gaa gaa 300
342 Leu Ile Ser Lys Gly Lys Ser Ser His Ile Leu Val Phe Asp Glu Glu
343 65 70 75 80
345 ctc ttc ttc att tac ctt ctt cct cca ata atc ttc aat gct ggg ttc 348
346 Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
347 85 90 95
349 caa gtt aag aaa aag aag ttt ttt cac aac ttt tta acc atc atg tcc 396

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 03/05/2001

PATENT APPLICATION: US/09/271,584A

TIME: 15:40:33

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1638

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/271,584A DATE: 02/22/2001
 TIME: 09:18:57

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**Does Not Comply
 Corrected Diskette Needed**

4 <110> APPLICANT: BLUMWALD, Eduardo
 5 APSE, Maris
 6 SNEDDEN, Wayne
 7 AHARON, Gilad
 9 <120> TITLE OF INVENTION: GENETIC ENGINEERING SALT TOLERANCE IN CROP PLANTS
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 12 <141> CURRENT FILING DATE: 1999-03-18
 14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00219
 15 <151> PRIOR FILING DATE: 1999-03-18
 17 <150> PRIOR APPLICATION NUMBER: US 60/078,474
 18 <151> PRIOR FILING DATE: 1998-04-01
 20 <150> PRIOR APPLICATION NUMBER: US 60/116,111
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ERRORED SEQUENCES

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↓
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 indicates. Sequences 17, 28 also
 were erred in this way.

VERIFICATION SUMMARY

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DATE: 02/22/2001

TIME: 09:18:58

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M:340 Repeated in SeqNo=23
L:1700 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1700 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1714 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1714 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1714 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:1716 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1716 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
M:340 Repeated in SeqNo=24
L:1717 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1727 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:1729 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1729 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1729 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1730 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1730 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:1734 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1734 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1735 M:252 E: No. of Seq. differs, <211>LENGTH:Input:0 Found:380 SEQ:25
L:1757 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1757 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1757 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1767 M:283 W: Missing Blank Line separator, <400> field identifier
L:1773 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:1773 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1773 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1790 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1790 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1790 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:1791 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1791 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
M:340 Repeated in SeqNo=28
L:1792 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1792 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1793 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1793 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1797 M:280 W: Numeric Identifier already exists, Length not replaced.
L:1798 M:280 W: Numeric Identifier already exists, Type not replaced.
L:1799 M:280 W: Numeric Identifier already exists, Organism not replaced.

VERIFICATION SUMMARY DATE: 02/22/2001
PATENT APPLICATION: US/09/271,584A TIME: 09:18:58

Input Set : A:\salt seq1stg.txt
Output Set: N:\CRF3\02222001\I271584A.raw

L:23 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (37) Counted (36)